

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Method of stabilizing protein solutions

<130> C1-A0319P

<150> JP 2003-351410

<151> 2003-10-09

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1779)

<223>

<400> 1

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Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

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gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag 96

Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Leu Val Gln

20 25 30

cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144

Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35 40 45

agc	agc	tgt	gcc	atg	agc	tgg	gtc	cgc	cag	gct	cca	ggg	aag	ggg	ctg	192	
Ser	Ser	Cys	Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu		
50															60		
gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca															240		
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala																	
65															75	80	
gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac															288		
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn																	
85															90	95	
acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta															336		
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val																	
100															105	110	
tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct															384		
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala																	
115															120	125	
tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc															432		
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala																	
130															135	140	
cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg															480		
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr																	
145															150	155	160
agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc															528		
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser																	
165															170	175	
atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc															576		
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr																	
180															185	190	

cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca	624		
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser			
195	200	205	
cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac	672		
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His			
210	215	220	
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg	720		
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val			
225	230	235	240
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc	768		
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val			
245	250	255	
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc	816		
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile			
260	265	270	
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg	864		
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu			
275	280	285	
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag	912		
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln			
290	295	300	
gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc acg aca	960		
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr			
305	310	315	320
ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc	1008		
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys			
325	330	335	
cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg	1056		

Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met			
340	345	350	
tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca			1104
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro			
355	360	365	
tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg			1152
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu			
370	375	380	
gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc			1200
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg			
385	390	395	400
cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac			1248
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His			
405	410	415	
ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat			1296
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp			
420	425	430	
gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac			1344
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp			
435	440	445	
ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc			1392
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala			
450	455	460	
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg			1440
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu			
465	470	475	480
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct			1488
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser			

485	490	495	
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc			1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
500	505	510	
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca			1584
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro			
515	520	525	
ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg			1632
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp			
530	535	540	
aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc			1680
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
545	550	555	560
aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc			1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
565	570	575	
ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac			1776
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
580	585	590	
tga			1779

<210> 2
 <211> 592
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
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 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Leu
 50 55 60
 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
 85 90 95
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
 115 120 125
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
 130 135 140
 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
 145 150 155 160
 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
 165 170 175
 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
 180 185 190
 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
 195 200 205
 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
 210 215 220
 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
 225 230 235 240
 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
 245 250 255
 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
 260 265 270
 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
 275 280 285
 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
 290 295 300
 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr

305	310	315	320
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys			
325	330	335	
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met			
340	345	350	
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro			
355	360	365	
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu			
370	375	380	
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg			
385	390	395	400
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His			
405	410	415	
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp			
420	425	430	
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp			
435	440	445	
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala			
450	455	460	
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu			
465	470	475	480
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser			
485	490	495	
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
500	505	510	
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro			
515	520	525	
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp			
530	535	540	
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
545	550	555	560
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
565	570	575	
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
580	585	590	

<210> 3

<211> 723

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(723)

<223>

<400> 3

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 1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96
 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192
 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr

100	105	110	
tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc 384 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr			
115	120	125	
aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc 432 Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe			
130	135	140	
ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc 480 Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys			
145	150	155	160
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg 528 Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val			
165	170	175	
gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag 576 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln			
180	185	190	
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc 624 Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser			
195	200	205	
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat 672 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His			
210	215	220	
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt 720 Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
225	230	235	240
tag 723			

<210> 4

<211> 240

<212> PRT

<213> Homo sapiens

<400> 4

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
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 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45
 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110
 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
 115 120 125
 Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 130 135 140
 Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 145 150 155 160
 Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 165 170 175
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 180 185 190
 Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 195 200 205
 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 210 215 220
 Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235 240

<210> 5
 <211> 480
 <212> DNA
 <213> Homo sapiens

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 <222> (1)..(480)
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 Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
 1 5 10 15

gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac 96
 Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
 20 25 30

aac aaa tgt aag tgt gcc cgg att act tcc agg atc atc cgt tct tcc 144
 Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
 35 40 45

gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt 192
 Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
 50 55 60

cct ctg aac aac agg gag aat atc tct gat ccc acc tca cca ttg aga 240
 Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
 65 70 75 80

acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct 288
 Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
 85 90 95

aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat 336

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
 100 105 110

atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga 384
 Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
 115 120 125

aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc 432
 Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
 130 135 140

aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa 480
 Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 145 150 155

<210> 6
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
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 Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
 20 25 30
 Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
 35 40 45
 Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
 50 55 60
 Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
 65 70 75 80
 Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
 85 90 95
 Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
 100 105 110
 Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg

115	120	125
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr		
130	135	140
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp		
145	150	155

<210> 7

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 7

ccaacggcaa caaagaaaaag aacg

24

<210> 8

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 8

aacatgcctc ggccgagcca gtcg

24

<210> 9

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 9

gcaagtccag ccagagtggtt ttat

24

<210> 10

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 10

ctgtccttgc tgtcctgctc tgtg

24

<210> 11

<211> 33

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 11

aacagctcga gccaccatgg agtttgggct gag

33

<210> 12

<211> 32

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 12

agcggccagc cgcccccagc ctgtcgacag gc

32

<210> 13

<211> 32

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 13

atagaattcc accatggtgt tgcagaccca gg

32

<210> 14

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 14

ggagcaggcg gccgcacttc tccctctaac

30

<210> 15

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 15

accattgaga accagatttg tgta

24

<210> 16

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 16

tgtgttagcac ttgtttctgt cata

24

<210> 17

<211> 28

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 17

atgaattcca ccatgaagaa ccatttg

28

<210> 18

<211> 26

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 18

tatctagatt agtcaggata gcaggc